

P200301025DK SEQ listing.ST25  
SEQUENCE LISTING

<110> Copenhagen University Tech Trans Enheden  
Mundy, John

<120> Plant disease resistance and SAR regulator protein

<130> P200301025

<160> 28

<170> PatentIn version 3.2

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<211> 669

<212> DNA

<213> Arabidopsis sp.

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<221> CDS

<222> (1)..(669)

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Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu	
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agt gtt cac aaa gac tct cac aaa atc aag aaa cct cca aaa cac cct	144
Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro	
35 40 45	
gcg ccg ccg cca aat cgt gac caa ccg ccg ccg tat att cct aga gag	192
Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu	
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ccg gtg gtt atc tac gcc gta tcc ccc aag gtt gta cac gca acc gcg	240
Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala	
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Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly	
85 90 95	
gtt ttc ctc gaa tct ggc ggc ggt gga gat gtt tca ccg gcg gcg agg	336
Val Phe Leu Glu Ser Gly Gly Gly Gly Asp Val Ser Pro Ala Ala Arg	
100 105 110	
cta gcg tcc acg gaa aat gct agt cca aga gga gga aaa gaa ccg gct	384
Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala	
115 120 125	
gcg aga gat gag acg gtg gaa atc aac acg gct atg gaa gaa gca gct	432
Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala	
130 135 140	
gaa ttt ggt ggt tat gct ccg gga ata ctc tcg cca tct ccg gcc ttg	480
Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu	
145 150 155 160	
ttg cca aca gct tct acc ggg ata ttc tct ccg atg tat cat caa ggt	528
Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly	
165 170 175	

## P200301025DK SEQ listing.ST25

ggg atg ttt tcg ccg gct ata cca ctg gga tta ttc tcg ccg gcg gga 576  
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ttt atg agc ccg ttt cga agt cct ggc ttt act agt ttg gta gct tca 624  
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Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro  
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Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu  
                   50                  55                  60

Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala  
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Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly  
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Val Phe Leu Glu Ser Gly Gly Gly Gly Asp Val Ser Pro Ala Ala Arg  
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Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala  
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Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala  
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Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu  
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Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly  
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Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly  
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## P200301025DK SEQ listing.ST25

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 20 25 30

cca cta gcg ccg cca cac ccg caa cca caa cca cca caa acc cat cag 144  
 Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln  
 35 40 45

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 Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr  
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tcc tat tct tca tct acg tca gca cca aaa gac gcg tca aca atg gtt 336  
 Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val  
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gat aca tct cat ggg ttg ata tct ccg gcg gct cgg ttt gct gtt aca 384  
 Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr  
 115 120 125

## P200301025DK SEQ listing.ST25

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 Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His Gln  
 145 150 155 160  
 gaa caa caa cat caa aat caa ggg ttc gag cgg cca agt ttc cac cat 528  
 Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His  
 165 170 175  
 gct ggg att tta tcg ccg gga cct aat tct ctg ccg tcg gta tca ccg 576  
 Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro  
 180 185 190  
 gac ttc ttt tcc act att gga cca acc gat cca caa ggt ttt tcg tcg 624  
 Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser  
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 210 215 220  
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 Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr  
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 Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr  
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 Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser  
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 Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val  
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 Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr  
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## P200301025DK SEQ listing.ST25

Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu  
130 135 140

Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His Gln  
145 150 155 160

Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His  
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Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro  
180 185 190

Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser  
195 200 205

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aactcttttg agaaaata atg gat ccg tcg gag tct ttc gcc ggc ggc aat 171  
Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn  
1 5 10

cct tcc gac caa cag aac cag aaa cgt cag ctt cag atc tgt ggt cct 219  
Pro Ser Asp Gln Gln Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro

## P200301025DK SEQ listing.ST25

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cct cct aaa cac cct gct cct ccg cct cag cat cgc gac caa gct ccg	Pro Pro Lys His Pro Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro	315	
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ctc tac gct gct cga gag ccg gtg gtc atc tac gcc gtc tcg ccg aaa	Leu Tyr Ala Ala Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys	363	
	60 65 70 75		
gtc gtc cac acc aca gcc tcg gat ttc atg aac gtc gtc cag cgt ctc	Val Val His Thr Thr Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu	411	
	80 85 90		
acc ggc atc tca tcc gcc gtc ttc ctc gaa tcc ggt aac ggc gga gat	Thr Gly Ile Ser Ser Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp	459	
	95 100 105		
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	110 115 120		
gga gga aaa gaa ccg gtg atg gcg gct aaa gat gag acg gtg gaa atc	Gly Gly Lys Glu Pro Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile	555	
	125 130 135		
gcg acg gct atg gaa gaa gca gcc gag ttg agc ggc tat gcg ccg ggg	Ala Thr Ala Met Glu Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly	603	
	140 145 150 155		
ata ctc tcc cct tct ccg gct atg tta ccg aca gct tct gcc gga ata	Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile	651	
	160 165 170		
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	175 180 185		
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ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro  
 35 40 45

## P200301025DK SEQ listing.ST25

Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro Leu Tyr Ala Ala Arg  
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Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr Thr  
65 70 75 80

Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser  
85 90 95

Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp Val Ser Pro Ala Ala  
100 105 110

Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro  
115 120 125

Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile Ala Thr Ala Met Glu  
130 135 140

Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser  
145 150 155 160

Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile Phe Ser Gln Met Thr  
165 170 175

Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu Phe Ser Pro Ala Gly  
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Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val Ala Ser Pro Thr Phe  
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<213> Brassica oleracea

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[illegible]



## P200301025DK SEQ listing.ST25

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Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Arg His Pro  
 35 40 45

Ala Pro Pro Pro Gln His His Arg Asp Gln Ala Pro Leu Tyr Pro Pro  
 50 55 60

Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr  
 65 70 75 80

Thr Thr Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser  
 85 90 95

Ser Glu Val Phe Leu Glu Ser Arg Asn Asp Gly Asp Val Ser Pro Ala  
 100 105 110

Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu  
 115 120 125

Pro Val Glu Ser Ser Thr Ala Met Glu Glu Ala Ala Glu Phe Gly Cys  
 130 135 140

Tyr Val Pro Gly Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Val  
 145 150 155 160

Pro Ala Gly Ile Phe Ser Pro Met Phe His Leu Gly Gly Leu Phe Ser  
 165 170 175

Pro Ala Leu Pro Pro Gly Leu Phe Ser Pro Ala Gly Leu Met Ser Pro  
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Gly Tyr Ala Ser Leu Ala Ser Pro Asn Phe Ala Asp Phe Phe Ser His  
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Ile Trp Asp Pro  
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 1 5 10 15  
 cat aaa atc aag aaa cca ccg ttg gca cca caa cct tca cac cct cat 96  
 His Lys Ile Lys Lys Pro Pro Leu Ala Pro Gln Pro Ser His Pro His  
 20 25 30  
 caa cct cca ccg cgc caa cct ata ata atc tac acc gtg tcc ccc aag 144  
 Gln Pro Pro Pro Arg Gln Pro Ile Ile Ile Tyr Thr Val Ser Pro Lys  
 35 40 45  
 gtg att cac acc acc cca agt gac ttc atg aac ctc gtc caa cgc ctc 192  
 Val Ile His Thr Thr Pro Ser Asp Phe Met Asn Leu Val Gln Arg Leu  
 50 55 60  
 act ggg tcc agt tct tct tcc tct gct gaa gtg gtc atg tcc aac aat 240  
 Thr Gly Ser Ser Ser Ser Ser Ser Ala Glu Val Val Met Ser Asn Asn  
 65 70 75 80  
 aac aac acc act cat gtc gac cct ttc aac aac ggc ggc ggc gga atg 288  
 Asn Asn Thr Thr His Val Asp Pro Phe Asn Asn Gly Gly Gly Gly Met  
 85 90 95  
 gtg tcg ccg gcg gcg cgt tac gcc acc ata gag aag gcc atg tcc cct 336  
 Val Ser Pro Ala Ala Arg Tyr Ala Thr Ile Glu Lys Ala Met Ser Pro  
 100 105 110  
 atg ggg aaa aaa cat gtt ctt ctt cca agt gtg aac aat att ata agc 384  
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 Asp Val Glu  
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 Gln Pro Pro Pro Arg Gln Pro Ile Ile Ile Tyr Thr Val Ser Pro Lys  
 35 40 45  
 Val Ile His Thr Thr Pro Ser Asp Phe Met Asn Leu Val Gln Arg Leu  
 50 55 60

## P200301025DK SEQ listing.ST25

Thr Gly Ser Ser Ser Ser Ser Ser Ala Glu Val Val Met Ser Asn Asn  
65 70 75 80

Asn Asn Thr Thr His Val Asp Pro Phe Asn Asn Gly Gly Gly Gly Met  
85 90 95

Val Ser Pro Ala Ala Arg Tyr Ala Thr Ile Glu Lys Ala Met Ser Pro  
100 105 110

Met Gly Lys Lys His Val Leu Leu Pro Ser Val Asn Asn Ile Ile Ser  
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Asp Val Glu  
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Ser Gly Gln His Gln Gln Gln Pro Thr Thr Pro Arg Arg Gln Leu Gln  
15 20 25 30

96

ggc ccg cgc ccc ccg cgg ctc aac gtg cgg atg gag tcg cac gcc atc  
Gly Pro Arg Pro 35 Arg Leu Asn Val Arg Met Glu Ser His Ala Ile  
40 45

144

aag aag ccg tcg tcc ggg gcg gcc gcg gcg gcg gcg gcg cag gcg  
Lys Lys Pro Ser Ser Gly Ala Ala 55 Ala Ala Ala Ala Ala Gln Ala  
50 60

192

agg cgg gag cag cag cag ccg ccg ccg cgg gcg ccg gtg atc atc tac  
240

## P200301025DK SEQ listing.ST25

Arg	Arg	Glu	Gln	Gln	Gln	Pro	Pro	Pro	Arg	Ala	Pro	Val	Ile	Ile	Tyr	
65						70						75				
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Asp	Ala	Ser	Pro	Lys	Ile	Ile	His	Ala	Lys	Pro	Asn	Glu	Phe	Met	Ala	
80						85					90					
ctc	gtg	cag	cgg	ctc	acc	ggc	ccg	ggg	tcg	ggg	ccg	ccg	gcg	ccg	ccg	336
Leu	Val	Gln	Arg	Leu	Thr	Gly	Pro	Gly	Ser	Gly	Pro	Pro	Ala	Pro	Pro	
95					100					105					110	
cat	caa	ggg	gag	gcc	cag	gcg	cag	gac	tac	ccg	atg	atg	gac	gag	gcc	384
His	Gln	Gly	Glu	Ala	Gln	Ala	Gln	Asp	Tyr	Pro	Met	Met	Asp	Glu	Ala	
				115					120					125		
gcc	gcg	cag	cag	ttc	ttc	ccg	ccg	gag	ctg	ctg	ctc	tcg	ccg	tcg	gcc	432
Ala	Ala	Gln	Gln	Phe	Phe	Pro	Pro	Glu	Leu	Leu	Leu	Ser	Pro	Ser	Ala	
				130				135					140			
gcg	atg	tcc	ccg	gcg	gcg	agg	ctg	gcg	acc	atc	gag	agg	tcc	gtc	cgc	480
Ala	Met	Ser	Pro	Ala	Ala	Arg	Leu	Ala	Thr	Ile	Glu	Arg	Ser	Val	Arg	
		145					150					155				
ccg	atg	ccc	gag	ccg	gcg	ccg	gag	tac	gtg	gac	atc	acg	aac	ggc	ggc	528
Pro	Met	Pro	Glu	Pro	Ala	Pro	Glu	Tyr	Val	Asp	Ile	Thr	Asn	Gly	Gly	
	160					165					170					
ggc	ggc	ggc	ggg	gtc	gac	gac	ggc	ggc	ctc	gcg	gcg	atc	ctc	ggc	tcg	576
Gly	Gly	Gly	Gly	Val	Asp	Asp	Gly	Gly	Leu	Ala	Ala	Ile	Leu	Gly	Ser	
175					180					185					190	
atc	cgg	cca	ggc	atc	ctc	tcc	ccg	ctc	ccc	tcc	tcc	ctc	ccg	ccc	gcc	624
Ile	Arg	Pro	Gly	Ile	Leu	Ser	Pro	Leu	Pro	Ser	Ser	Leu	Pro	Pro	Ala	
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gcc	gtc	ccc	ggc	cag	ttc	tcg	ccg	ctc	ccg	ttc	gac	gcg	agg	ccg	ctc	672
Ala	Val	Pro	Gly	Gln	Phe	Ser	Pro	Leu	Pro	Phe	Asp	Ala	Arg	Pro	Leu	
			210					215					220			
ccg	ttc	gac	gcg	agc	tgc	atc	agc	tgg	ctc	aac	gag	ctg	agc	ccc	atc	720
Pro	Phe	Asp	Ala	Ser	Cys	Ile	Ser	Trp	Leu	Asn	Glu	Leu	Ser	Pro	Ile	
		225					230					235				
ctc	cgg	gcc	gcc	tcc	gcc	ggc	gcg	gcc	tcg	tcc	ggc	agc	ggc	ggc	ggc	768
Leu	Arg	Ala	Ala	Ser	Ala	Gly	Ala	Ala	Ser	Ser	Gly	Ser	Gly	Gly	Gly	
	240					245					250					
ggc	agc	ggt	ggc	aac	acc	agc	aac	ggc	ggc	ggc	gcc	cgc	ccg	ccg	ccg	816
Gly	Ser	Gly	Gly	Asn	Thr	Ser	Asn	Gly	Gly	Gly	Ala	Arg	Pro	Pro	Pro	
255					260				265						270	
tcc	tac	tac	gcc	gac	cca	ttc	gtc	ccc	agc	cca	cgt	cac	ctc	ctc	gcc	864
Ser	Tyr	Tyr	Ala	Asp	Pro	Phe	Val	Pro	Ser	Pro	Arg	His	Leu	Leu	Ala	
				275					280					285		
acg	ccc	acc	gtg	ccg	tcg	ccg	gcg	acc	tgc	gcc	gag	ctc	ttc	agc	aac	912
Thr	Pro	Thr	Val	Pro	Ser	Pro	Ala	Thr	Cys	Ala	Glu	Leu	Phe	Ser	Asn	
			290					295					300			
ctg	ccg	gat	ctc	tag												927
Leu	Pro	Asp	Leu													
		305														

<210> 20  
 <211> 306  
 <212> PRT  
 <213> Oryza sp.

## P200301025DK SEQ listing.ST25

&lt;400&gt; 20

Met Glu Phe Pro Ser Ser Thr Ser Pro Ser Pro Ser Pro Ser Ser Gly  
 1 5 10 15

Gln His Gln Gln Gln Pro Thr Thr Pro Arg Arg Gln Leu Gln Gly Pro  
 20 25 30

Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His Ala Ile Lys Lys  
 35 40 45

Pro Ser Ser Gly Ala Ala Ala Ala Ala Ala Ala Gln Ala Arg Arg  
 50 55 60

Glu Gln Gln Gln Pro Pro Pro Arg Ala Pro Val Ile Ile Tyr Asp Ala  
 65 70 75 80

Ser Pro Lys Ile Ile His Ala Lys Pro Asn Glu Phe Met Ala Leu Val  
 85 90 95

Gln Arg Leu Thr Gly Pro Gly Ser Gly Pro Pro Ala Pro Pro His Gln  
 100 105 110

Gly Glu Ala Gln Ala Gln Asp Tyr Pro Met Met Asp Glu Ala Ala Ala  
 115 120 125

Gln Gln Phe Phe Pro Pro Glu Leu Leu Leu Ser Pro Ser Ala Ala Met  
 130 135 140

Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg Ser Val Arg Pro Met  
 145 150 155 160

Pro Glu Pro Ala Pro Glu Tyr Val Asp Ile Thr Asn Gly Gly Gly Gly  
 165 170 175

Gly Gly Val Asp Asp Gly Gly Leu Ala Ala Ile Leu Gly Ser Ile Arg  
 180 185 190

Pro Gly Ile Leu Ser Pro Leu Pro Ser Ser Leu Pro Pro Ala Ala Val  
 195 200 205

Pro Gly Gln Phe Ser Pro Leu Pro Phe Asp Ala Arg Pro Leu Pro Phe  
 210 215 220

Asp Ala Ser Cys Ile Ser Trp Leu Asn Glu Leu Ser Pro Ile Leu Arg  
 225 230 235 240

Ala Ala ser Ala Gly Ala Ala Ser Ser Gly Ser Gly Gly Gly Gly Ser  
 245 250 255

Gly Gly Asn Thr Ser Asn Gly Gly Gly Ala Arg Pro Pro Pro Ser Tyr  
 Page 13

## P200301025DK SEQ listing.ST25

260

265

270

Tyr Ala Asp Pro Phe Val Pro Ser Pro Arg His Leu Leu Ala Thr Pro  
 275 280 285

Thr Val Pro Ser Pro Ala Thr Cys Ala Glu Leu Phe Ser Asn Leu Pro  
 290 295 300

Asp Leu  
 305

<210> 21  
 <211> 16  
 <212> DNA  
 <213> Oryza sp.

<400> 21  
 atggaattcc cgtcgt

16

<210> 22  
 <211> 19  
 <212> DNA  
 <213> Oryza sp.

<400> 22  
 ctagagatcc ggcaggttg

19

<210> 23  
 <211> 781  
 <212> DNA  
 <213> CaMV 35S promoter duplicated

<400> 23  
 atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac 60  
 caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat 120  
 tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaagggtg cacctacaaa 180  
 tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtgggtccc 240  
 aaagatggac cccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct 300  
 tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag 360  
 aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta 420  
 atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca 480  
 gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt 540  
 caagatgcct ctgccgacag tgggtcccaa gatggacccc caccacgag gagcatcgtg 600  
 gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact 660  
 gacgtaaggg atgacgcaca atcccactat ccttcgcaag accttcctct atataaggaa 720  
 gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc 780  
 t 781

## P200301025DK SEQ listing.ST25

<210> 24  
 <211> 253  
 <212> DNA  
 <213> Agrobacterium NOS terminator

<400> 24  
 cgttcaaaca ttggaata aagtttctta agattgaatc ctgttgccgg tcttgcatg 60  
 attatcatat aatttctggt gaattacggt aagcatgtaa taattaacat gtaatgcatg 120  
 acgttattta tgagatgggt ttttatgatt agagtccgc aattatacat ttaatacgcg 180  
 atagaaaaca aaatatagcg cgcaaactag gataaattat cgcgcgcggg gtcattctatg 240  
 ttactagatc ggg 253

<210> 25  
 <211> 189  
 <212> DNA  
 <213> Synthetic intron

<400> 25  
 gtaagtttct gcttctacct ttgatataata tataataatt atcattaatt agtagtaata 60  
 taatatttca aatatttttt tcaaaataaa agaattgtagt atatagcaat tgcttttctg 120  
 tagtttataa gtgtgtatat ttttaatttat aacttttcta atatatgacc aaaatttgtt 180  
 gatgtgcag 189

<210> 26  
 <211> 207  
 <212> PRT  
 <213> Oryza sp.

<400> 26  
 Met Glu Gln Gln Leu Ser Ser Pro Ser Ala Ser Gln Arg Gly Gly Gly 15  
 1 5 10  
 Arg Glu Leu Gln Gly Pro Arg Pro Ala Pro Leu Lys Val Arg Lys Glu 30  
 20 25 30  
 Ser His Lys Ile Arg Lys Gln Glu Pro Val Gln Gln Leu Arg Gln Pro 45  
 35 40 45  
 Val Ile Ile Tyr Thr Met Ser Pro Lys Val Val His Ala Asn Ala Ala 60  
 50 55 60  
 Asp Phe Met Ser Val Val Gln Arg Leu Thr Gly Ala Pro Pro Thr Ala 80  
 65 70 75 80  
 Pro Pro Gln Pro Gln Pro His His Pro Thr Leu Leu Ala Gln Met Pro 95  
 85 90 95  
 Pro Gln Pro Ser Phe Pro Phe His Leu Gln Gln Gln Asp Ala Trp Pro 110  
 100 105 110  
 Gln Gln Gln His Ser Pro Ala Ala Ile Glu Gln Ala Ala Ala Arg Ser  
 Page 15

## P200301025DK SEQ listing.ST25

115

120

125

Ser Gly Ala Asp Leu Pro Pro Leu Pro Ser Ile Leu Ser Pro Val Pro  
 130 135 140

Gly Thr Val Leu Pro Ala Ile Pro Ala Ser Phe Phe Ser Pro Pro Ser  
 145 150 155 160

Leu Ile Ser Pro Val Pro Phe Leu Gly Ala Thr Thr Thr Ser Ser Ala  
 165 170 175

Ala Pro Ser Thr Ser Pro Ser Pro Met Gly Gly Ser Ala Tyr Tyr Trp  
 180 185 190

Asp Leu Phe Asn Met Gln Gln Gln Gln His Tyr His His Gln Asn  
 195 200 205

<210> 27  
 <211> 238  
 <212> PRT  
 <213> Zea mays

<400> 27

Met Asp Pro Pro Ser Ser Ser Gly Arg Pro Thr Thr Pro Arg Arg Gln  
 1 5 10 15

Leu Gln Gly Pro Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His  
 20 25 30

Ala Ile Lys Lys Pro Ser Ala Ser Gly Ala Pro Pro Ala Pro Gly Gln  
 35 40 45

Gly Arg Pro Arg Asp His His His His His Pro Gln Pro Gly Arg Ala  
 50 55 60

Pro Val Ile Ile Tyr Asp Ala Ser Pro Lys Val Ile His Ala Lys Pro  
 65 70 75 80

Ser Glu Phe Met Ala Leu Val Gln Arg Leu Thr Gly Pro Gly Ala Gln  
 85 90 95

Ala Gln His Glu Arg His Val Ala Asp Asp Asp Ala Thr Ala Asn Gly  
 100 105 110

Gly Gly Val Leu Gly Gln Ala Phe Leu Pro Pro Glu Leu Leu Leu Ser  
 115 120 125

Pro Ser Ala Ala Met Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg  
 130 135 140

Ser Val Arg Pro Val Pro Ala Pro Ala Pro Ala Pro Asp Tyr Ala Ala  
 145 150 155 160



## P200301025DK SEQ Listing.ST25

Asp Gly His Pro Arg Gly Gly Ala Arg Pro Arg Glu Ala Pro Arg His  
 165 170 175  
 Pro Val Pro Ala Ala Val Leu Ala Ala Ala Gly Arg Arg Val Gly Pro  
 180 185 190  
 Val Leu Ala Ala Ala Leu Arg Pro Gln Gln Arg Gln Leu Ala Gln Arg  
 195 200 205  
 Ala Gln Pro His Pro Pro Gly Ser Val His Gly Gln Arg Ser Ala Pro  
 210 215 220  
 Leu Ala His Ala His Gly Pro Thr Gly Gly Ser Arg Gln Pro  
 225 230 235  
 <210> 28  
 <211> 271  
 <212> PRT  
 <213> Zea mays  
 <400> 28  
 Gln Gly Pro Arg Pro Pro Arg Leu Ala Val Ser Lys Asp Ser His Lys  
 1 5 10 15  
 Val Arg Lys Pro Pro Val Ala Pro Gln Arg Gln Gln His Gln His Gln  
 20 25 30  
 Gln Pro Ala Ala Gln Leu Gln Gln Gln His Gln Tyr His Gln Gln  
 35 40 45  
 Gln Gln Gln Gln Gly Arg Gln Pro Val Ile Ile Tyr Asp Ala Ser Pro  
 50 55 60  
 Lys Val Ile His Thr Lys Pro Gly Asp Phe Met Ala Leu Val Gln Arg  
 65 70 75 80  
 Leu Thr Gly Pro Gly Ser Thr Ser Gln Ala Gln Phe Asp Ala Ala Ala  
 85 90 95  
 Ala Ala Ala Gly Pro Ser His Pro Ala Ala Met Glu Phe Glu Pro Arg  
 100 105 110  
 Glu Phe Leu Leu Ser Pro Thr Ala Ala Leu Ser Pro Ala Ala Arg Leu  
 115 120 125  
 Ala Ala Ile Glu Arg Ser Val Arg Pro Leu Pro Pro His His Ala Pro  
 130 135 140  
 Ala Ala Val Pro Pro Tyr Phe Gly Ala Thr Asn Asp Asp Gly Phe Phe  
 145 150 155 160

## P200301025DK SEQ listing.ST25

Leu Pro Gly Ser Ala Asp Met Asp Ser Leu Ser Ala Ala Leu Gly Pro  
165 170 175

Pro Ala Gly Arg Pro Gly Ile Leu Ser Pro Ala Ala Leu Pro Pro Ala  
180 185 190

Ala Ser Thr Gly Leu Phe Ser Pro Met Pro Phe Asp Pro Ser Cys Leu  
195 200 205

Ser Trp Leu Ser Glu Leu Ser Pro Phe Leu Pro Ser Ala Gly Thr Arg  
210 215 220

Ala Ala Ala Ala Gly Leu Leu Asp Gln Ala Pro Phe Ala Pro Ser Pro  
225 230 235 240

Arg Ser Ser Leu Leu Leu Ser Thr Pro Thr Met Pro Ser Pro Ala Thr  
245 250 255

Phe Ser Val Leu Glu Phe Phe Ser Ser Pro Asn Phe Pro Asp Leu  
260 265 270